

#16



## RAW SEQUENCE LISTING

DATE: 05/24/2002

PATENT APPLICATION: US/09/671,658A

TIME: 09:44:30

Input Set : N:\Crf3\RULE60\09671658A.RAW

Output Set: N:\CRF3\05242002\I671658A.raw

## SEQUENCE LISTING

3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: Gorman, Daniel M.

6 Mattson, Jeanine D.

8 (ii) TITLE OF INVENTION: Mammalian Cell Surface Antigens; Related

9 Reagents

11 (iii) NUMBER OF SEQUENCES: 2

13 (iv) CORRESPONDENCE ADDRESS:

14 (A) ADDRESSEE: DNAX Research Institute

15 (B) STREET: 901 California Avenue

16 (C) CITY: Palo Alto

17 (D) STATE: California

18 (E) COUNTRY: USA

19 (F) ZIP: 94304-1104

21 (v) COMPUTER READABLE FORM:

22 (A) MEDIUM TYPE: Floppy disk

23 (B) COMPUTER: IBM PC compatible

24 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

25 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

27 (vi) CURRENT APPLICATION DATA:

C--> 28 (A) APPLICATION NUMBER: US/09/671,658A

C--> 29 (B) FILING DATE: 27-Sep-2000

30 (C) CLASSIFICATION:

32 (vii) PRIOR APPLICATION DATA:

34 (A) APPLICATION NUMBER: US/08/989,362

35 (B) FILING DATE: 12-DEC-1997

37 (A) APPLICATION NUMBER: US 60/032,846

38 (B) FILING DATE: 13-DEC-1996

40 (viii) ATTORNEY/AGENT INFORMATION:

41 (A) NAME: Ching, Edwin P.

42 (B) REGISTRATION NUMBER: 34,090

43 (C) REFERENCE/DOCKET NUMBER: DX0686

45 (ix) TELECOMMUNICATION INFORMATION:

46 (A) TELEPHONE: (650)852-9196

47 (B) TELEFAX: (650)496-1204

50 (2) INFORMATION FOR SEQ ID NO: 1:

52 (i) SEQUENCE CHARACTERISTICS:

53 (A) LENGTH: 2191 base pairs

54 (B) TYPE: nucleic acid

55 (C) STRANDEDNESS: single

56 (D) TOPOLOGY: linear

58 (ii) MOLECULE TYPE: cDNA

61 (ix) FEATURE:

ENTERED

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62      (A) NAME/KEY: CDS
63      (B) LOCATION: 125..1072
66      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
68 GCCAGGACCT CTGTGAACCG GTCGGGGCGG GGGCCGCCTG GCCGGGAGTC TGCTCGGCGG      60
70 TGGGTGGCCG AGGAAGGGAG AGAACGATCG CGGAGCAGGG CGCCCGAACT CCGGGCGCCG      120
72 CGCC ATG CGC CGG GCC AGC CGA GAC TAC GGC AAG TAC CTG CGC AGC TCG      169
73      Met Arg Arg Ala Ser Arg Asp Tyr Gly Lys Tyr Leu Arg Ser Ser
74      1          5          10          15
76 GAG GAG ATG GGC AGC GGC CCC GGC GTC CCA CAC GAG GGT CCG CTG CAC      217
77 Glu Glu Met Gly Ser Gly Pro Gly Val Pro His Glu Gly Pro Leu His
78      20          25          30
80 CCC GCG CCT TCT GCA CCG GCT CCG GCG CCG CCA CCC GCC GCC TCC CGC      265
81 Pro Ala Pro Ser Ala Pro Ala Pro Ala Pro Pro Pro Ala Ala Ser Arg
82      35          40          45
84 TCC ATG TTC CTG GCC CTC CTG GGG CTG GGA CTG GGC CAG GTG GTC TGC      313
85 Ser Met Phe Leu Ala Leu Leu Gly Leu Gly Leu Gly Gln Val Val Cys
86      50          55          60
88 AGC ATC GCT CTG TTC CTG TAC TTT CGA GCG CAG ATG GAT CCT AAC AGA      361
89 Ser Ile Ala Leu Phe Leu Tyr Phe Arg Ala Gln Met Asp Pro Asn Arg
90      65          70          75
92 ATA TCA GAA GAC AGC ACT CAC TGC TTT TAT AGA ATC CTG AGA CTC CAT      409
93 Ile Ser Glu Asp Ser Thr His Cys Phe Tyr Arg Ile Leu Arg Leu His
94      80          85          90          95
96 GAA AAC GCA GGT TTG CAG GAC TCG ACT CTG GAG AGT GAA GAC ACA CTA      457
97 Glu Asn Ala Gly Leu Gln Asp Ser Thr Leu Glu Ser Glu Asp Thr Leu
98      100          105          110
100 CCT GAC TCC TGC AGG AGG ATG AAA CAA GCC TTT CAG GGG GCC GTG CAG      505
101 Pro Asp Ser Cys Arg Arg Met Lys Gln Ala Phe Gln Gly Ala Val Gln
102      115          120          125
104 AAG GAA CTG CAA CAC ATT GTG GGG CCA CAG CGC TTC TCA GGA GCT CCA      553
105 Lys Glu Leu Gln His Ile Val Gly Pro Gln Arg Phe Ser Gly Ala Pro
106      130          135          140
108 GCT ATG ATG GAA GGC TCA TGG TTG GAT GTG GCC CAG CGA GGC AAG CCT      601
109 Ala Met Met Glu Gly Ser Trp Leu Asp Val Ala Gln Arg Gly Lys Pro
110      145          150          155
112 GAG GCC CAG CCA TTT GCA CAC CTC ACC ATC AAT GCT GCC AGC ATC CCA      649
113 Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Ala Ser Ile Pro
114      160          165          170          175
116 TCG GGT TCC CAT AAA GTC ACT CTG TCC TCT TGG TAC CAC GAT CGA GGC      697
117 Ser Gly Ser His Lys Val Thr Leu Ser Ser Trp Tyr His Asp Arg Gly
118      180          185          190
120 TGG GCC AAG ATC TCT AAC ATG ACG TTA AGC AAC GGA AAA CTA AGG GTT      745
121 Trp Ala Lys Ile Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg Val
122      195          200          205
124 AAC CAA GAT GGC TTC TAT TAC CTG TAC GCC AAC ATT TGC TTT CGG CAT      793
125 Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His
126      210          215          220
128 CAT GAA ACA TCG GGA AGC GTA CCT ACA GAC TAT CTT CAG CTG ATG GTG      841
129 His Glu Thr Ser Gly Ser Val Pro Thr Asp Tyr Leu Gln Leu Met Val

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130      225      230      235
132 TAT GTC GTT AAA ACC AGC ATC AAA ATC CCA AGT TCT CAT AAC CTG ATG      889
133 Tyr Val Val Lys Thr Ser Ile Lys Ile Pro Ser Ser His Asn Leu Met
134 240      245      250      255
136 AAA GGA GGG AGC ACG AAA AAC TGG TCG GGC AAT TCT GAA TTC CAC TTT      937
137 Lys Gly Gly Ser Thr Lys Asn Trp Ser Gly Asn Ser Glu Phe His Phe
138      260      265      270
140 TAT TCC ATA AAT GTT GGG GGA TTT TTC AAG CTC CGA GCT GGT GAA GAA      985
141 Tyr Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ala Gly Glu Glu
142      275      280      285
144 ATT AGC ATT CAG GTG TCC AAC CCT TCC CTG CTG GAT CCG GAT CAA GAT      1033
145 Ile Ser Ile Gln Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp
146      290      295      300
148 GCG ACG TAC TTT GGG GCT TTC AAA GTT CAG GAC ATA GAC TGAGACTCAT      1082
149 Ala Thr Tyr Phe Gly Ala Phe Lys Val Gln Asp Ile Asp
150      305      310      315
152 TTCGTGGAAC ATTAGCATGG ATGTCCTAGA TGTTTGGAAA CTTCTTAAAA AATGGATGAT      1142
154 GTCTATACAT GTGTAAGACT ACTAAGAGAC ATGGCCCACG GTGTATGAAA CTCACAGCCC      1202
156 TCTCTCTTGA GCCTGTACAG GTTGTGTATA TGTAAGTCC ATAGGTGATG TTAGATTCAT      1262
158 GGTGATTACA CAACGGTTTT ACAATTTTGT AATGATTTC TAAGAATTGA ACCAGATTGG      1322
160 GAGAGGTATT CCGATGCTTA TGAAAACTT ACACGTGAGC TATGGAAGGG GGTCACAGTC      1382
162 TCTGGGTCTA ACCCTGGAC ATGTGCCACT GAGAACCCTG AAATTAAGAA GATGCCATGT      1442
164 CATTGCAAAG AATGATAGT GTGAAGGGT AAGTCTTTT GAATTGTTAC ATTGCGCTGG      1502
166 GACCTGCAAA TAAGTTCTTT TTTTCTAATG AGGAGAGAAA AATATATGTA TTTTATATA      1562
168 ATGTCTAAAG TTATATTTCA GGTGTAATGT TTTCTGTGCA AAGTTTGTGA AATTATATTT      1622
170 GTGCTATAGT ATTTGATTCA AAATATTTAA AAATGTCTCA CTGTTGACAT ATTTAATGTT      1682
172 TTAAATGTAC AGATGTATTT AACTGGTGCA CTTTGTAATT CCCCTGAAGG TACTCGTAGC      1742
174 TAAGGGGGCA GAATACTGTT TCTGGTGACC ACATGTAGTT TATTTCTTTA TTCTTTTAA      1802
176 CTTAATAGAG TCTTCAGACT TGCAAAACT ATGCAAGCAA AATAAATAAA TAAAAATAAA      1862
178 ATGAATATCT TGAATAATAA GTAGGATGTT GGTCACCAGG TGCCTTCAA ATTTAGAAGC      1922
180 TAATTGACTT TAGGAGCTGA CATAGCCAAA AAGGATACAT AATAGGCTAC TGAAAATCTG      1982
182 TCAGGAGTAT TTATGCAATT ATTGAACAGG TGTCTTTTTT TACAAGAGCT ACAAATTGTA      2042
184 AATTTTGTGT CTTTTTTTTC CCATAGAAAA TGTACTATAG TTTATCAGCC AAAAAACAAT      2102
186 CCACTTTTTA ATTTAGTGAA AGTTATTTTA TTATACTGTA CAATAAAAGC ATTGTTTCTG      2162
188 AATGGCATTT TTTGGTACTT AAAAATGGC      2191
191 (2) INFORMATION FOR SEQ ID NO: 2:
193 (i) SEQUENCE CHARACTERISTICS:
194 (A) LENGTH: 316 amino acids
195 (B) TYPE: amino acid
196 (D) TOPOLOGY: linear
198 (ii) MOLECULE TYPE: protein
200 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
202 Met Arg Arg Ala Ser Arg Asp Tyr Gly Lys Tyr Leu Arg Ser Ser Glu
203 1      5      10      15
205 Glu Met Gly Ser Gly Pro Gly Val Pro His Glu Gly Pro Leu His Pro
206      20      25      30
208 Ala Pro Ser Ala Pro Ala Pro Ala Pro Pro Pro Ala Ala Ser Arg Ser
209      35      40      45
211 Met Phe Leu Ala Leu Leu Gly Leu Gly Leu Gly Gln Val Val Cys Ser

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212      50      55      60
214 Ile Ala Leu Phe Leu Tyr Phe Arg Ala Gln Met Asp Pro Asn Arg Ile
215 65      70      75      80
217 Ser Glu Asp Ser Thr His Cys Phe Tyr Arg Ile Leu Arg Leu His Glu
218      85      90      95
220 Asn Ala Gly Leu Gln Asp Ser Thr Leu Glu Ser Glu Asp Thr Leu Pro
221      100      105      110
223 Asp Ser Cys Arg Arg Met Lys Gln Ala Phe Gln Gly Ala Val Gln Lys
224      115      120      125
226 Glu Leu Gln His Ile Val Gly Pro Gln Arg Phe Ser Gly Ala Pro Ala
227      130      135      140
229 Met Met Glu Gly Ser Trp Leu Asp Val Ala Gln Arg Gly Lys Pro Glu
230 145      150      155      160
232 Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Ala Ser Ile Pro Ser
233      165      170      175
235 Gly Ser His Lys Val Thr Leu Ser Ser Trp Tyr His Asp Arg Gly Trp
236      180      185      190
238 Ala Lys Ile Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg Val Asn
239      195      200      205
241 Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His His
242      210      215      220
244 Glu Thr Ser Gly Ser Val Pro Thr Asp Tyr Leu Gln Leu Met Val Tyr
245 225      230      235      240
247 Val Val Lys Thr Ser Ile Lys Ile Pro Ser Ser His Asn Leu Met Lys
248      245      250      255
250 Gly Gly Ser Thr Lys Asn Trp Ser Gly Asn Ser Glu Phe His Phe Tyr
251      260      265      270
253 Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ala Gly Glu Glu Ile
254      275      280      285
256 Ser Ile Gln Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp Ala
257      290      295      300
259 Thr Tyr Phe Gly Ala Phe Lys Val Gln Asp Ile Asp
260 305      310      315

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VERIFICATION SUMMARY

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L:28 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:29 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]